

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:02:18 : Search time 11.2654 seconds
(without alignments)
2282.679 Million cell updates/sec

Title: US-10-054-680-4
3228
Perfect score: 1 MAWLRQLQPLRSALFLHFLVLT.....ADYGRRGQEDSRDCKASIG 620
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3093	95.8	595	1	NAC3_HUMAN
2	3016	93.4	927	1	NAC3_RAT
3	2159.5	66.9	970	1	P23685 canis faml
4	2152.5	66.7	970	1	NAC1_CANFA
5	2147.5	66.5	970	1	NAC1_BOVIN
6	2146.5	66.5	973	1	NAC1_HUMAN
7	2142.5	66.4	970	1	NAC1_CAVPO
8	2135.5	66.2	971	1	NAC1_RAT
9	2115.5	65.5	970	1	NAC1_MOUSE
10	1961	60.7	921	1	NAC2_HUMAN
11	1954.5	60.5	921	1	NAC2_RAT
12	209.5	6.5	663	1	NKX1_CHICK
13	203.5	6.3	661	1	NKX2_HUMAN
14	203	6.3	1181	1	NKX1_RAT
15	201.5	6.2	670	1	NKX2_RAT
16	199.5	6.2	651	1	NKX2_CHICK
17	194.5	6.0	1216	1	NKX1_BOVIN
18	186.5	5.8	644	1	NKX3_HUMAN
19	181	5.6	624	1	NKX3_RAT
20	179	5.5	645	1	NKX3_MOUSE
21	178	5.5	1099	1	NKX1_HUMAN
22	162.5	5.0	856	1	NKX3_DROME
23	141.5	4.4	572	1	YRT4_CAEEL
24	132	4.1	1807	1	YRT4_RAT
25	131	4.1	590	1	YRT4_CAEEL
26	126.5	3.9	1822	1	ITB4_HUMAN
27	110	3.4	3358	1	PCGV_MOUSE
28	108	3.3	673	1	COAT_PAVBO
29	107	3.3	548	1	CH60_EHRSE
30	107	3.3	649	1	TOP3_SALTI
31	106.5	3.3	1036	1	YAN2_SCHPO
32	106	3.3	649	1	TOP3_SALTY
33	105.5	3.3	548	1	CH60_EHRI

34	105	3.3	402	1	PGK_CHLUP
35	104.5	3.2	686	1	MAP2_MOUSE
36	104.5	3.2	1828	1	MAP2_MOUSE
37	103.5	3.2	988	1	TNP6_ENTFC
38	102.5	3.2	2009	1	CINI_HUMAN
39	101.5	3.1	989	1	RPOC_LEUME
40	100	3.1	1065	1	SEC8_YEAST
41	99.5	3.1	1018	1	SVL_ARCFU
42	98.5	3.1	558	1	RFL_YEAST
43	97.5	3.0	558	1	TCPE_THAVE
44	97.5	3.0	803	1	RIRI_CRYPV
45	97	3.0	1254	1	UBPC_YEAST

ALIGNMENTS

RESULT 1	ID	NAME	STANDARD	PRT	595 AA
NAC3_HUMAN	1	NAC3_HUMAN	STANDARD	PRT	595 AA
AC	P57103	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein 3) (Fragment).				
GN	SLC8A3	OR NCX3.			
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kreev A.S., Chumakov I.M., Carafoli E.				
RT	"The organization of the human gene of the sodium-calcium exchanger.";				
RL	Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.				
CC	- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION				
CC	COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS				
CC	TO PREVENT OVERLOADING OF INTRACELLULAR STORES (BY SIMILARITY).				
CC	- ENZYME REGULATION: BY INTRACELLULAR CALCIUM IONS (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib.ch).				
CC	-----				
DR	EMBL	X93017	;	NOT_ANNOTATED_CDS.	
DR	Gene	HGNC:11070	;	SLC8A3.	
DR	InterPro	IPR003644	;	Calx_beta.	
DR	InterPro	IPR004837	;	Naca_Exmemb.	
DR	InterPro	IPR004836	;	Na_Ca_Ex.	
DR	Pfam	PF01699	;	Na_Ca_Ex.1.	
DR	Pfam	PF03160	;	Calx_beta.2.	
DR	SMART	SM00237	;	Calx_beta.2.	
DR	TIGRFAMs	TIGR00845	;	caca.1.	
KW	Transport: Antiport; Calcium transport; Sodium transport;				
KW	Transmembrane; Glycoprotein; Phosphorylation; Signal;				
KW	Calmodulin-binding; Repeat.				
FT	SIGNAL	1	30		POTENTIAL.
FT	CHAIN	31	>595		SODIUM/CALCIUM EXCHANGER 3.
FT	DOMAIN	31	73		EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	74	94		POTENTIAL.
FT	TRANSMEM	95	147		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	148	168		POTENTIAL.
FT	DOMAIN	169	169		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	170	190		POTENTIAL.
FT	DOMAIN	191	202		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	203	223		POTENTIAL.
FT	DOMAIN	224	230		EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 231 251 POTENTIAL.
FT DOMAIN 252 >595 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 595 595
SQ SEQUENCE 595 AA; 66238 MW; 5DE30D649ACEB5BA CRC64;

Query Match 95.8%; Score 3093; DB 1; Length 595;
Best Local Similarity 100.0%; Pred. No. 9.5e-216;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMRLRQPLTSARLHGLVTVFLNLGLRAAGSGDVPSTGONNESCSSDCKEGVIL 60
DB 1 MAMRLRQPLTSARLHGLVTVFLNLGLRAAGSGDVPSTGONNESCSSDCKEGVIL 60
QY 61 PIWPEPNSLGDKIARIYVFAVLIYFVLGVSIIADRFMAISIEVTSQEREVITKKNGE 120
DB 61 PIWPEPNSLGDKIARIYVFAVLIYFVLGVSIIADRFMAISIEVTSQEREVITKKNGE 120
QY 121 TSTTTIVWNETVSNLTLMALGSSAPILLSLIEVCGHGTIAGDLGPSTIVGSAFNMFT 180
DB 121 TSTTTIVWNETVSNLTLMALGSSAPILLSLIEVCGHGTIAGDLGPSTIVGSAFNMFT 180
QY 181 IIGICVAVIDGGETRKIKHLRVFETIAMSIFATIMLTAVSPGVQVWEGLLTLFF 240
DB 181 IIGICVAVIDGGETRKIKHLRVFETIAMSIFATIMLTAVSPGVQVWEGLLTLFF 240
QY 241 FPCVLLAVYADKRLLFYKFMKKRTDKRGIIIEFGDHPKGIEMDGKMMNSHFLDGN 300
DB 241 FPCVLLAVYADKRLLFYKFMKKRTDKRGIIIEFGDHPKGIEMDGKMMNSHFLDGN 300
QY 301 LVPEGEVDESREMITRIIKLQKHPEKDLDOLVEMANYALSHOOKSRAFRIGQTR 360
DB 301 LVPEGEVDESREMITRIIKLQKHPEKDLDOLVEMANYALSHOOKSRAFRIGQTR 360
QY 361 MMTGAGNIIKKHAEQKKAASSMEVHTDEPEDEISKVFEPDPSYQCLEMGCAVLTIVR 420
DB 361 MMTGAGNIIKKHAEQKKAASSMEVHTDEPEDEISKVFEPDPSYQCLEMGCAVLTIVR 420
QY 421 KGGDMSKTMVVDYKTEDEGSANAGADYEFTGTVLKPGETQKEFSVGIIIDDIFFEEDEHF 480
DB 421 KGGDMSKTMVVDYKTEDEGSANAGADYEFTGTVLKPGETQKEFSVGIIIDDIFFEEDEHF 480
QY 481 FVRLSNVRIEEOPEEEMPAIFNSLPLPRAVLASPCVATVTTIIDDHAGIIFFECDTIH 540
DB 481 FVRLSNVRIEEOPEEEMPAIFNSLPLPRAVLASPCVATVTTIIDDHAGIIFFECDTIH 540
QY 541 VSESIGVMEVKVLTSGARGTVIYFRTVGTAKGGGEDEEDYTGELFEKNDETV 595
DB 541 VSESIGVMEVKVLTSGARGTVIYFRTVGTAKGGGEDEEDYTGELFEKNDETV 595

RESULT 2
NAC3 RAT STANDARD: PRT: 927 AA.
AC P70549;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein 3).
GN SLC8A3 OR NCX3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=96394663; PubMed=8798769;
RA MEDLI D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA Philpson K.D.;
RT *Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.*;
RL J. Biol. Chem. 271:24914-24921(1996).

CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
CC COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY INTRACELLULAR CALCIUM IONS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSION RESTRICTED TO BRAIN AND SKELETAL
CC MUSCLE.
CC -----
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CC -----
DR EMBL: U53420; AAC52817.1; -.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF01699; NaCa_Ex; 2.
DR Pfam: PF03160; Calx_beta; 2.
DR PRINTS: PR01259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRPFAMS: TIGR00845; caca; 1.
KW Transport; Antiport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT STGNAL 1 30
FT CHAIN 1 927
FT DOMAIN 31 927
FT TRANSSEM 31 73
FT DOMAIN 74 94
FT TRANSSEM 95 147
FT TRANSSEM 148 168
FT DOMAIN 169 190
FT TRANSSEM 170 190
FT DOMAIN 191 202
FT TRANSSEM 203 223
FT DOMAIN 224 230
FT TRANSSEM 231 251
FT DOMAIN 252 276
FT TRANSSEM 727 747
FT DOMAIN 748 754
FT TRANSSEM 755 775
FT DOMAIN 776 778
FT TRANSSEM 779 799
FT TRANSSEM 800 828
FT TRANSSEM 829 849
FT DOMAIN 850 860
FT TRANSSEM 861 881
FT TRANSSEM 882 903
FT TRANSSEM 904 924
FT TRANSSEM 925 927
FT DOMAIN 253 272
FT REPEAT 140 180
FT REPEAT 399 470
FT REPEAT 534 604
FT REPEAT 796 832
FT DOMAIN 645 648
FT CARBOHYD 45 45
FT CARBOHYD 823 823
SQ SEQUENCE 927 AA; 103162 MW; EAB35F9620DBE69E CRC64;

Query Match 93.4%; Score 3016; DB 1; Length 927;
Best Local Similarity 97.1%; Pred. No. 6.3e-210;
Matches 578; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAMRLRQPLTSARLHGLVTVFLNLGLRAAGSGDVPSTGONNESCSSDCKEGVIL 60
DB 1 MAMRLRQPLTSARLHGLVTVFLNLGLRAAGSLDVPSTGONNESCSSDCKEGVIL 60
QY 61 PIWPEPNSLGDKIARIYVFAVLIYFVLGVSIIADRFMAISIEVTSQEREVITKKNGE 120

Db 117 GETTATVIRINNEVYNSLTLMLAGSSAPEILLSVIEVGHNTFADLGPSTIVGSAAFNM 176

Qy 179 FIIIGICVYVDPDGETRKIKLRVFFITPAAMSTFAYILMYLMLAVSPGVQVWEGGLTL 238

Db 177 FIIMACVYVDPDGETRKIKLRVFFITPAAMSTFAYILMYLMLAVSPGVQVWEGGLTLF 236

Qy 239 FEPFACVLLAWADVDRLLFYKYMHHKRYPRDKHRIIIEEGDHPKG---IEMDGKMMNSH 295

Db 237 FEPFICVFAWADVDRLLFYKRYRGRGKGMIIIEEGDRPSSKTEIEMDGKVVNSH 296

Qy 296 ---FLDGNLVLPLEGKVD---ESRREMIRILDKOKHPEKLDQLTEMANYVALSHQQ 348

Db 297 VDNFLDGLALV-LEVDERODDEARREMARILKELKOKHPEKIEQILIELANYQVLSQQQ 355

Qy 349 KSRAFYRIQATRMATGAGNIIKKHAAEQAKKASMSSEVHTDEP-DFISKVEFDPCSYQC 407

Db 356 KSRAFYRIQATRIKMGAGNIIKRNHAADARKAIVSMHEVNTVEVAENDPVSKIFFEGGTQC 415

Qy 408 LENCAGVLLTVRKGGDKSMKYVYVKPEDGSANMGADYEFTEGTVLKRPGTOKEFSVG 467

Db 416 LENCSTVATLTIRKGGDLNTVYFVFRLEDGTANAGSDTEFEGTVKRPGETOKEIRVG 475

Qy 468 IIDDIFEEDEHFFRLSNVRIIEEQDPEEGMPAIFNSLPLRAVLASPCVATVITLDD 527

Db 476 IIDDIFEEDEHFFRLSNVRIIEEQDPEEGMPAIFNSLPLRAVLASPCVATVITLDD 532

Qy 528 HAGITFECDTIVHSESIGVMEVKVLRITSGARGVIVFPRVETGAKGGEDFEDTYGEL 587

Db 533 HAGITFECDTIVHSESIGVMEVKVLRITSGARGVIVFPRVETGAKGGEDFEDTYGEL 592

Qy 588 EFKNDETV 595

Db 593 EFKNDETV 600

RESULT 4

NACL_FELCA

ID NACL_FELCA STANDARD: PRT: 970 AA.

AC P48767; P79174;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).

GN SLC8A1 OR NCX1.

OS Fells silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.

OX NCBI_TaxId=9685;

PN [1]

SEQUENCE FROM N.A.

NC TISSUE=Heart;

RX MEDLINE=96250114; Pubmed=8659865;

RA Menick D.R., Barnes K.V., Thacker U.F., Dawson M.M., McErmott D.E., Rozlich J.D., Kent R.L., Cooper G.; "The exchanger and cardiac hypertrophy"; Ann. N.Y. Acad. Sci. 779:489-501(1996).

RL [2]

RP SEQUENCE OF 1-600 FROM N.A.

RX MEDLINE=97269065; Pubmed=9111065;

RA Barnes K.V., Cheng G., Dawson M.M., Menick D.R.; "Cloning of cardiac, kidney, and brain promoters of the feline ncx1 gene."; J. Biol. Chem. 272:11510-11517(1997).

RT -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.

CC -1- ENZYME REGULATION: BY ATP.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.

CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA.

CC -----

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[illegible]

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Db 116 NGETTATVTRIMNETVSNLTLMLALGSSAPEILLVIEVCHGNFTAGDLGPSTIVGSAFN 175
Qy 178 MFTIIGCVYIIPDGEFRKIKHLVFFTTAAMSIFATIMLMLAVSPGVQVWEGILLT 237
Db 176 MFTIIGCVYIIPDGEFRKIKHLVFFTTAAMSIFATIMLMLAVSPGVQVWEGILLT 235
Qy 238 LEFPVVCVLAVMDKRLLEFKYKMKHKYKRDKHGIIETEGDHPKGS--ITEMGKMNS 294
Db 236 FFEPPICVAFVAVMDKRLLEFKYKMKHKYKRDKHGIIETEGDHPKGS--ITEMGKMNS 295
Qy 295 H---FLDGNLVLEKGEVD---ESRREMRILKDLKOKHPEKDLQVEMANYATLSHQ 347
Db 296 HDVNFPLDGLALV-LEVDERNDQDEARREMARILKELKHKEKELEQILANQVLSQ 354
Qy 348 OKSAPFRIRIQAQTRMTGAGNLIKHAAEQAKKASSMSEVHTDEP-DFISVFEFDPGSG 406
Db 355 OKSAPFRIRIQAQTRMTGAGNLIKHAADQAKKASSMSEVHTDEP-DFISVFEFDPGSG 414
Qy 407 CLENGAVLTVKRGKGMSTMYVDYKTEGDSANAGADYFETGTVVLKRGTEQKESY 466
Db 415 CLENGAVLTVKRGKGMSTMYVDYKTEGDSANAGADYFETGTVVLKRGTEQKESY 474
Qy 467 GIIDDIFEEDEHFEVRLSNVRIEEOPEEGMPAIFNSLPLPRAVLASPCVATYTIID 526
Db 475 GIIDDIFEEDEHFEVRLSNVRIEEOPEEGMPAIFNSLPLPRAVLASPCVATYTIID 531
Qy 527 DHAGIFFECDTIVSESIGVEKVLRTSGAGTVIPEFTVECTAGGSEDEPTYGE 586
Db 532 DHAGIFFECDTIVSESIGVEKVLRTSGAGTVIPEFTVECTAGGSEDEPTYGE 591
Qy 587 LEKNDENV 595
Db 592 LEFONDELIV 600

RESULT 5
NACL_BOVIN
ID NACL_BOVIN STANDARD; PRT: 970 AA.
AC P48765;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
  1).
GN SLC8A1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
  Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX
RN
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Heart;
RC MEDLINE=93037494; PubMed=1416984;
RA Aceto J.F., Condrescu M., Kroupis C., Nelson H., Nelson N.,
  Nicoll D.A., Philipson K.D., Reeves J.P.;
RT "Cloning and expression of the bovine cardiac sodium-calcium
  exchanger.";
RT Arch. Biochem. Biophys. 298:553-560(1992).
RN
RN [2]
RN SUBCELLULAR LOCATION.
RC TISSUE=Retinal rod cell;
RC MEDLINE=90241959; PubMed=2334719;
RA Reid D.M., Friedel U., Molday R.S., Cook N.J.;
RT "Identification of the sodium-calcium exchanger as the major
  riclin-binding glycoprotein of bovine rod outer segments and its
  localization to the plasma membrane.";
RT Biochemistry 29:1601-1607(1990).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
  SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.

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CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL: L06438; AAA30509.1; -.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; Na_Ca_Ex.
DR Pfam: PF01699; Na_Ca_Ex; 2.
DR Pfam: PF03160; Calx_beta; 2.
DR PRINTS: PR01259; NACAECHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
DR Transport; Antipor; Calcium
KW Transport; Antipor; Calcium
KW Calmodulin-binding; Repeat.
FT SIGNAL 1 32
FT CHAIN 33 970
FT DOMAIN 33 71
FT TRANSSEM 72 93
FT DOMAIN 94 133
FT TRANSSEM 134 155
FT DOMAIN 156 167
FT TRANSSEM 168 188
FT DOMAIN 189 199
FT TRANSSEM 200 222
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 FT VARSPLIC 605 613 TISKVYDD -> IITRIDRD (IN ISOFORM 3, ISOFORM 7 AND ISOFORM 10).
 FT VARSPLIC 619 645 NKTFELTEGEPRLEEMSEKRALLENEL -> EGSFSLVEE PKMIRGKM (IN ISOFORM 3, ISOFORM 7 AND ISOFORM 10).
 FT VARSPLIC 652 656 MISSING (IN ISOFORM 7).
 FT VARSPLIC 652 679 MISSING (IN ISOFORM 3).
 FT SEQUENCE 973 AA: 108546 MW: 17061815921D8 CRC64:
 Query Match 66.5%; Score 2146.5; DB 1; Length 973;
 Best Local Similarity 69.2%; Pred. No. 4, 1e-147;
 Matches 421; Conservative 76; Mismatches 90; Indels 21; Gaps 8;

ID NACL_CAVPO STANDARD; PRT; 970 AA.
 AC P48766;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).
 GN SLC8A1.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Caviidae; Cavia.
 OX NCBI_Taxid=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95078257; PubMed=7986817;
 RA Tsunura Y., Bersohn M.M., Li Z., Nicoll D.A., Philipson K.D.;
 RT "Molecular cloning and functional expression of the guinea pig cardiac Na(+)-Ca2+ exchanger."
 RT Biochim. Biophys. Acta 1196:97-99(1994).
 RL -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
 CC -1- ENZYME REGULATION: BY ATP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA.
 CC -----
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 CC -----
 DR EMBL: U04955; AAA73904.1; -
 DR InterPro: IPR003644; calx_beta.
 DR InterPro: IPR004837; NaCa_Exmemb.
 DR InterPro: IPR004836; NaCa_Ex.
 DR Pfam: PF01699; NaCa_Ex; 2.
 DR Pfam: PF03160; Calx_beta; 2.
 DR PRINTS: PR01259; NACAEXCHNGR.
 DR SMART: SM00237; Calx_beta; 2.
 DR TIGRFAMs: TIGR00845; beta; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport; Transmembrane; Glycoprotein; Calmodulin-binding; Repeat.
 KW KW
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
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 FT TRANSMEM 942 958 POTENTIAL.
 FT DOMAIN 959 970 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 970 970 CALMODULIN-BINDING (POTENTIAL).
 FT DOMAIN 251 270

RESULT 7
 NACL_CAVPO

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FT REPEAT 138 178 ALPHA-1.
FT REPEAT 407 478 BETA-1.
FT REPEAT 539 609 BETA-2.
FT REPEAT 839 875 ALPHA-2.
FT DOMAIN 236 239 POLY-PHE.
FT DOMAIN 689 692 POLY-GLU.
FT DOMAIN 756 760 POLY-ASP.
FT MOD.RES 389 389 PHOSPHORYLATION (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 970 AA: 108071 MW: 720364C8BD157739 C6C64;

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Query Match 66.4%; Score 2142.5; DB 1: Length 970;
Best Local Similarity 69.1%; Pred. No. 7.9e-147;
Matches 420; Conservative 76; Mismatches 91; Indels 21; Gaps 9;

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OY 1 MAMLRLOPLTSARLH-FGLVTPVL-FLNGRAEAGSGDVPSTGQNNSSGSSDCKEY 58
DB 1 MLRLSPPTYSGLCFHLLAMTTLISHVDHTAET---EKVEGNETGECTGSYKKG 56
OY 59 ILPTWPNPNSLDKTAIVYVVALIYMEFGVSIADRFMASIEVITSOEREVTIKRP 118
DB 57 ILPIWPOPSGDKIARATVYVAVMYVMEFGVSIADRFMSIEVITSOEREVTIKRP 116
OY 119 GETSTTIRVWNETVSNLTALMGSSAPELLISLIEVCGHGFIAGDLGPSTIVGSAFNN 178
DB 117 GETTKTIVRWNETVSNLTALMGSSAPELLISLIEVCGHGFIAGDLGPSTIVGSAFNN 176
OY 179 FIITGCVVPIPDGETRKRKLHLEVFITAAWSTFAVIMYLAVSPGVVWBEILLT 238
DB 177 FIITACVVPVDPGETRKRKLHLEVFITAAWSTFAVIMYLAVSPGVVWBEILLT 236
OY 239 FEPPVCVLLAWADKRLFLFYKMHKKYRTDKHNGIIEEGDHPKC---IEMDGKMMNSH 295
DB 237 FEPPICVFAWVADKRLFLFYKMHKKYRTDKHNGIIEEGDHPKC---IEMDGKMMNSH 296
OY 296 ---FLDGNLPLLEGKEVD---ESREMRILKDKOKRPEKLDOLVEMANYALSHQ 348
DB 297 VENFDLGAIV-LEVDRDDDEAREMARILKELKOKRPEKLEOLIELANQVLSQO 355
OY 349 KSRAPRIQATRMGTAGNLIKKAHQAOKKASMEVHTDEPE-PEFISVFPDPCSYC 407
DB 356 KSRAPRIQATRMGTAGNLIKKAHQAOKKASMEVHTDEPE-PEFISVFPDPCSYC 415
OY 408 LENCAGVLLTVKRGKDMSTMYDYKTEBDGSANAGADYEFTGTVLKPGETOKESYVG 467
DB 416 LENCAGVLLTVKRGKDMSTMYDYKTEBDGSANAGADYEFTGTVLKPGETOKESYVG 475
OY 468 IIDDIDFEDEHFFVLSNVRIEEOPEEGMPPAIRNSLPLPAVLASPCVATVTLLDD 527
DB 476 IIDDIDFEDEHFFVLSNVRIEEOPEEGMPPAIRNSLPLPAVLASPCVATVTLLDD 532
OY 528 HAGIFTECDTIVHSESGIMEYKVLRTSGARGTIVPRTVGEKGGGEDEDTYGEI 587
DB 533 HAGIFTECDTIVHSESGIMEYKVLRTSGARGTIVPRTVGEKGGGEDEDTYGEI 592
OY 588 EFKNDETV 595
DB 593 EFKNDETV 600

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=9338118; PubMed=8422940;
RT Low W., Kasir J., Rahamimoff H.;
RT "Cloning of the rat heart Na(+) -Ca2+ exchanger and its functional
RL expression in HeLa cells.";
RL FEBS Lett. 316:63-67(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RA MEDLINE=9320224; PubMed=8454039;
RT Furan I., Cook O., Kasir J., Rahamimoff H.;
RT "Cloning of two isoforms of the rat brain Na(+) -Ca2+ exchanger gene
RT and their functional expression in HeLa cells.";
RL FEBS Lett. 319:105-109(1993).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney cortex;
RA MEDLINE=9425303; PubMed=8195112;
RT Lee S.-L., Yu A.S.L., Lytton J.;
RT "Tissue-specific expression of Na(+) -Ca2+ exchanger isoforms.";
RL J. Biol. Chem. 269:14849-14852(1994).
RN [4]
RP TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley;
RA MEDLINE=96394663; PubMed=8798769;
RT Nicoll D.A., Quedrau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA Phillipson K.D.;
RT "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
RL J. Biol. Chem. 271:24914-24921(1996).
CC -I- FUNCTION: RAPIDLY IS EXTRUDED FROM THE CELL DURING RELAXATION
CC COUPLING. CA(2+) ARE PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -I- ENZYME REGULATION: BY ATP.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -I- ALTERNATIVE PRODUCTS: 5 isoforms: heart/NCA1 (shown here),
CC brain 1/NACA5, brain 2/NACA4, kidney 1/NCAV and kidney 2/NACA3;
CC are produced by alternative splicing.
CC -I- TISSUE SPECIFICITY: CARDIAC SARCOLEMA OR BRAIN, AND SPLEEN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X68191; CAA48273.1; -
DR EMBL: X68812; CAA48707.1; -
DR EMBL: X68813; CAA48708.1; -
DR EMBL: U04933; AAB39952.1; -
DR EMBL: U04934; AAA19124.1; -
DR EMBL: U04936; AAA19125.1; -
DR PIR: S2552; S2552.
DR PIR: S28833; S28833.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmnd.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF01699; NaCa_Ex; 2.
DR Pfam: PF03160; Calx_beta; 2.
DR PRINTS: PR01259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TRIGRAMS: TRIGR00845; caca; 1.
DR Transmembrane; Antiport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat; Alternative splicing.
FT SIGNAL 1 32
FT CHAIN 33 971 SODIUM/CALCIUM EXCHANGER 1.

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FT	DOMAIN	33	71	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	72	93	POTENTIAL.
FT	DOMAIN	94	133	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	134	135	POTENTIAL.
FT	TRANSMEM	156	167	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	168	188	POTENTIAL.
FT	TRANSMEM	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	TRANSMEM	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	TRANSMEM	250	770	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	771	790	POTENTIAL.
FT	TRANSMEM	791	797	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	798	820	POTENTIAL.
FT	TRANSMEM	821	822	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	823	841	POTENTIAL.
FT	TRANSMEM	842	872	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	873	893	POTENTIAL.
FT	TRANSMEM	894	904	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	905	925	POTENTIAL.
FT	TRANSMEM	926	942	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	943	959	POTENTIAL.
FT	TRANSMEM	960	971	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	972	977	POTENTIAL.
FT	TRANSMEM	978	983	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	984	990	POTENTIAL.
FT	TRANSMEM	991	1000	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1001	1010	POTENTIAL.
FT	TRANSMEM	1011	1020	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1021	1030	POTENTIAL.
FT	TRANSMEM	1031	1040	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1041	1050	POTENTIAL.
FT	TRANSMEM	1051	1060	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1061	1070	POTENTIAL.
FT	TRANSMEM	1071	1080	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1081	1090	POTENTIAL.
FT	TRANSMEM	1091	1100	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1101	1110	POTENTIAL.
FT	TRANSMEM	1111	1120	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1121	1130	POTENTIAL.
FT	TRANSMEM	1131	1140	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1141	1150	POTENTIAL.
FT	TRANSMEM	1151	1160	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1161	1170	POTENTIAL.
FT	TRANSMEM	1171	1180	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1181	1190	POTENTIAL.
FT	TRANSMEM	1191	1200	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1201	1210	POTENTIAL.
FT	TRANSMEM	1211	1220	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1221	1230	POTENTIAL.
FT	TRANSMEM	1231	1240	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1241	1250	POTENTIAL.
FT	TRANSMEM	1251	1260	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1261	1270	POTENTIAL.
FT	TRANSMEM	1271	1280	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1281	1290	POTENTIAL.
FT	TRANSMEM	1291	1300	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1301	1310	POTENTIAL.
FT	TRANSMEM	1311	1320	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1321	1330	POTENTIAL.
FT	TRANSMEM	1331	1340	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1341	1350	POTENTIAL.
FT	TRANSMEM	1351	1360	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1361	1370	POTENTIAL.
FT	TRANSMEM	1371	1380	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1381	1390	POTENTIAL.
FT	TRANSMEM	1391	1400	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1401	1410	POTENTIAL.
FT	TRANSMEM	1411	1420	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1421	1430	POTENTIAL.
FT	TRANSMEM	1431	1440	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1441	1450	POTENTIAL.
FT	TRANSMEM	1451	1460	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1461	1470	POTENTIAL.
FT	TRANSMEM	1471	1480	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1481	1490	POTENTIAL.
FT	TRANSMEM	1491	1500	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1501	1510	POTENTIAL.
FT	TRANSMEM	1511	1520	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1521	1530	POTENTIAL.
FT	TRANSMEM	1531	1540	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1541	1550	POTENTIAL.
FT	TRANSMEM	1551	1560	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1561	1570	POTENTIAL.
FT	TRANSMEM	1571	1580	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1581	1590	POTENTIAL.
FT	TRANSMEM	1591	1600	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1601	1610	POTENTIAL.
FT	TRANSMEM	1611	1620	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1621	1630	POTENTIAL.
FT	TRANSMEM	1631	1640	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1641	1650	POTENTIAL.
FT	TRANSMEM	1651	1660	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1661	1670	POTENTIAL.
FT	TRANSMEM	1671	1680	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1681	1690	POTENTIAL.
FT	TRANSMEM	1691	1700	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1701	1710	POTENTIAL.
FT	TRANSMEM	1711	1720	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1721	1730	POTENTIAL.
FT	TRANSMEM	1731	1740	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1741	1750	POTENTIAL.
FT	TRANSMEM	1751	1760	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1761	1770	POTENTIAL.
FT	TRANSMEM	1771	1780	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1781	1790	POTENTIAL.
FT	TRANSMEM	1791	1800	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1801	1810	POTENTIAL.
FT	TRANSMEM	1811	1820	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1821	1830	POTENTIAL.
FT	TRANSMEM	1831	1840	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1841	1850	POTENTIAL.
FT	TRANSMEM	1851	1860	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1861	1870	POTENTIAL.
FT	TRANSMEM	1871	1880	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1881	1890	POTENTIAL.
FT	TRANSMEM	1891	1900	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1901	1910	POTENTIAL.
FT	TRANSMEM	1911	1920	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1921	1930	POTENTIAL.
FT	TRANSMEM	1931	1940	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1941	1950	POTENTIAL.
FT	TRANSMEM	1951	1960	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1961	1970	POTENTIAL.
FT	TRANSMEM	1971	1980	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1981	1990	POTENTIAL.
FT	TRANSMEM	1991	2000	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2001	2010	POTENTIAL.
FT	TRANSMEM	2011	2020	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2021	2030	POTENTIAL.
FT	TRANSMEM	2031	2040	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2041	2050	POTENTIAL.
FT	TRANSMEM	2051	2060	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2061	2070	POTENTIAL.
FT	TRANSMEM	2071	2080	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2081	2090	POTENTIAL.
FT	TRANSMEM	2091	2100	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2101	2110	POTENTIAL.
FT	TRANSMEM	2111	2120	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2121	2130	POTENTIAL.
FT	TRANSMEM	2131	2140	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2141	2150	POTENTIAL.
FT	TRANSMEM	2151	2160	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2161	2170	POTENTIAL.
FT	TRANSMEM	2171	2180	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2181	2190	POTENTIAL.
FT	TRANSMEM	2191	2200	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2201	2210	POTENTIAL.
FT	TRANSMEM	2211	2220	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2221	2230	POTENTIAL.
FT	TRANSMEM	2231	2240	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2241	2250	POTENTIAL.
FT	TRANSMEM	2251	2260	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2261	2270	POTENTIAL.
FT	TRANSMEM	2271	2280	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2281	2290	POTENTIAL.
FT	TRANSMEM	2291	2300	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2301	2310	POTENTIAL.
FT	TRANSMEM	2311	2320	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2321	2330	POTENTIAL.
FT	TRANSMEM	2331	2340	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2341	2350	POTENTIAL.
FT	TRANSMEM	2351	2360	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2361	2370	POTENTIAL.
FT	TRANSMEM	2371	2380	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2381	2390	POTENTIAL.
FT	TRANSMEM	2391	2400	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2401	2410	POTENTIAL.
FT	TRANSMEM	2411	2420	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2421	2430	POTENTIAL.
FT	TRANSMEM	2431	2440	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2441	2450	POTENTIAL.
FT	TRANSMEM	2451	2460	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2461	2470	POTENTIAL.
FT	TRANSMEM	2471	2480	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2481	2490	POTENTIAL.
FT	TRANSMEM	2491	2500	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2501	2510	POTENTIAL.
FT	TRANSMEM	2511	2520	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2521	2530	POTENTIAL.
FT	TRANSMEM	2531	2540	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2541	2550	POTENTIAL.
FT	TRANSMEM	2551	2560	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2561	2570	POTENTIAL.
FT	TRANSMEM	2571	2580	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2581	2590	POTENTIAL.
FT	TRANSMEM	2591	2600	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2601	2610	POTENTIAL.
FT	TRANSMEM	2611	2620	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2621	2630	POTENTIAL.
FT	TRANSMEM	2631	2640	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2641	2650	POTENTIAL.
FT	TRANSMEM	2651	2660	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2661	2670	POTENTIAL.
FT	TRANSMEM	2671	2680	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2681	2690	POTENTIAL.
FT	TRANSMEM	2691	2700	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2701	2710	POTENTIAL.
FT	TRANSMEM	2711	2720	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2721	2730	POTENTIAL.
FT	TRANSMEM	2731	2740	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2741	2750	POTENTIAL.
FT	TRANSMEM	2751	2760	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2761	2770	POTENTIAL.
FT	TRANSMEM	2771	2780	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2781	2790	POTENTIAL.
FT	TRANSMEM	2791	2800	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2801	2810	POTENTIAL.
FT	TRANSMEM	2811	2820	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2821	2830	POTENTIAL.
FT	TRANSMEM	2831	2840	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2841	2850	POTENTIAL.
FT	TRANSMEM	2851	2860	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2861	2870	POTENTIAL.
FT	TRANSMEM	2871	2880	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2881	2890	POTENTIAL.
FT	TRANSMEM	2891	2900	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2901	2910	POTENTIAL.
FT	TRANSMEM	2911	2920	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2921	2930	POTENTIAL.
FT	TRANSMEM	2931	2940	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2941	2950	POTENTIAL.
FT	TRANSMEM	2951	2960	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2961	2970	POTENTIAL.
FT	TRANSMEM	2971	2980	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	2981	2990	POTENTIAL.
FT	TRANSMEM	2991	3000	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3001	3010	POTENTIAL.
FT	TRANSMEM	3011	3020	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3021	3030	POTENTIAL.
FT	TRANSMEM	3031	3040	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3041	3050	POTENTIAL.
FT	TRANSMEM	3051	3060	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3061	3070	POTENTIAL.
FT	TRANSMEM	3071	3080	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3081	3090	POTENTIAL.
FT	TRANSMEM	3091	3100	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3101	3110	POTENTIAL.
FT	TRANSMEM	3111	3120	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3121	3130	POTENTIAL.
FT	TRANSMEM	3131	3140	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3141	3150	POTENTIAL.
FT	TRANSMEM	3151	3160	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3161	3170	POTENTIAL.
FT	TRANSMEM	3171	3180	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3181	3190	POTENTIAL.
FT	TRANSMEM	3191	3200	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3201	3210	POTENTIAL.
FT	TRANSMEM	3211	3220	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3221	3230	POTENTIAL.
FT	TRANSMEM	3231	3240	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3241	3250	POTENTIAL.
FT	TRANSMEM	3251	3260	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3261	3270	POTENTIAL.
FT	TRANSMEM	3271	3280	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3281	3290	POTENTIAL.
FT	TRANSMEM	3291	3300	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3301	3310	POTENTIAL.
FT	TRANSMEM	3311	3320	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3321	3330	POTENTIAL.
FT	TRANSMEM	3331	3340	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3341	3350	POTENTIAL.
FT	TRANSMEM	3351	3360	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3361	3370	POTENTIAL.
FT	TRANSMEM	3371	3380	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3381	3390	POTENTIAL.
FT	TRANSMEM	3391	3400	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	3401		

Oy	293	NSH -FLDGNLVPLEGK-EVD- ---ESREMRIRILKLDKQHPKEDDLQVLVEMANYALS	345
Dd	294	NSHDNFLEIDGALV -LEVDERODDOBEAREMARRIIKELKHDPKEIQLIELANYOYLS	352
Oy	346	HOKSRATFYRLOATMMTGAGNIIKKHAHEOAKKASSSEVHTDEPE -DFISKYFFDDPCS	404
Dd	353	OOKSRAFRYRIOATPLMGTAGNIIKRHAADQARKVASHVENMDVENDPVSKVFEEGGT	412
Oy	405	YQCLENCAVALLTJVVRKGGMDSKITWYVDYKTJEDGSANAGADEPTEGTAVLKPGETOEK	464
Dd	413	YQCLENCTVAITLTRRGCDLNTNFVFPRTEDGTANAGSDYEFEFGTVIFKPGETOEKI	472
Oy	465	SVGITIDDIDEDEFERFRLSNVRIEEOGPREGMPRAFNLSP.LPLR -AIVLASPCATVTI	523
Dd	473	RGIITDDIFEDEDENEFLHLNSNRSSSEVSDEG---ILLDSNHSAICLCSPNTATTITI	528
Oy	524	LDDDHAGIFTFECDCDIHVESIGIVEVYLVRTSGARGTVIYPFTVEGTAKGGGEDEDT	583
Dd	529	FDDDHAGIFTFEREPYTHYSESISGINEVAVLVLRTSGRGVNIIPYKTIESTANGGDPEDET	588
Oy	584	YGEEFKNDDEVY 595 :	
Dd	589	CGELEFONDEITY 600	

RESULT 9

ID	NCBI_MOUSE	STANDARD;	PRT;	970 AA.
AC	P70414:			
Dt	01-NOV-1997 (Rel. 35, Created)			
Dt	01-NOV-1997 (Rel. 35, Last sequence update)			
Dt	15-JUN-2002 (Rel. 41, Last annotation update)			
De	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein			
De	1).			
GN	SLC8A1 OR NCX.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
Ox	NCBI_Taxid=10090;			
Rn	[1]			
Rp	SEQUENCE FROM N.A.,			
Rc	STRAIN=C57BL/6;			
Rx	MEDLINE=96250070; Pubmed=8659820;			
Ra	Kim I., Lee C.O.;			
Rt	"Cloning of the mouse cardiac Na(+)-Ca ²⁺ exchanger and functional			
Rl	expression in Xenopus oocytes."			
An	Ann. N.Y. Acad. Sci. 779:126-128,(1996).			
-1-	FUNCTION: RAPIDLY TRANSPORTS CA ²⁺ DURING EXCITATION-CONTRACTION			
CC	COUPLING. CA ²⁺ IS EXTRUDED FROM THE CELL DURING RELAXATION			
CC	SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.			
-1-	ENZYM REGULATION: BY ATP.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.			
CC	-1- TISSUE SPECIFICITY: CARDIAC SARCOLEMMA.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U70033; AAB46708.1; -.			
DR	MGP: MGI:107956; Slc8a1.			
DR	InterPro: IPR0033644; Calx_beta.			
DR	InterPro: IPR004837; NaCa_Exmemb.			
DR	InterPro: IPR004836; Na_Ca_Ex.			
DR	pfam: PF01699; Na_Ca_Ex_2.			
DR	pfam: PF03160; calx-beta; 2.			
DR	PRINTS: PR01259; NAACAEXCHNR.			
DR	SMART: SM00237; Calx_beta; 2.			
DR	TIGRFAMs: TIGR00845; caca; 1.			
Kw	Transport; Calcium transport; Sodium transport;			

FT	DOMAIN	91	130	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	131	152	POTENTIAL.
FT	DOMAIN	153	164	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	165	185	POTENTIAL.
FT	DOMAIN	186	196	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	197	219	POTENTIAL.
FT	DOMAIN	220	222	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	223	246	POTENTIAL.
FT	DOMAIN	247	720	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	721	740	POTENTIAL.
FT	DOMAIN	741	747	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	748	770	POTENTIAL.
FT	DOMAIN	771	772	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	773	791	POTENTIAL.
FT	DOMAIN	792	822	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	823	843	POTENTIAL.
FT	DOMAIN	844	854	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	855	875	POTENTIAL.
FT	DOMAIN	876	892	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	893	909	POTENTIAL.
FT	DOMAIN	910	921	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	248	267	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	135	175	ALPHA-1.
FT	REPEAT	397	468	BETA-1.
FT	REPEAT	527	597	BETA-2.
FT	REPEAT	790	826	ALPHA-2.
FT	DOMAIN	29	32	POLY-PRO.
FT	DOMAIN	638	641	POLY-GLU.
FT	CARBOHYD	34	34	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	817	817	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	921 AA:	100367 MW:	998CSF7E32B9410C CRC64;

Query Match	60.7%	Score 1961	DB 1	Length 921
Best Local Similarity	65.7%	Pred. No. 9.3e-134		
Matches 371	Conservative 87	Mismatches 83	Indels 24	Gaps
QY	40	STGQNNESCSSSDCKEGVLLPIWYENPSLGDKIARIYVFAVLIYMFGLSVSIIDRFM	99	
Db	39	STG-----CGCGSYRCQPCVLLPWVEBPDDSLGDKAARAVYFVAMVYMFGLSVSIIDRFM	94	
QY	100	ASIEVITSGEHEVITIKRNGESTSTTIRKMYEIVYSNLTMAAGSAPILLSLIEVCGHG	155	
Db	95	AAIEVITSKKEEITITKANGSETSVGIVKIMETVSNLTMAAGSAPILLSLIEVYEGHN	154	
QY	160	FIAGLGPSTIVGSAAFMFIIIGICVYIPDGETRKIKHLRVPEITAAANSIFAYITLYM	219	
b	155	FOAGLGGGTIVGSAAFMFYVIAVCITVIPAGESRKIKHLRVFFVAYIAMSIFAYVLYL	214	
QY	220	ILAVFSPGVVOWEGLLTLFFPVCVLLAWADKRLFFYKMKKRYRTDKHGIITETG	279	
Db	215	ILAVFSPGVVOWEALLTLVFFPCVAVFAMADKRLFFYKVKRYRRDPGSIIGIAGG	274	
QY	280	DHPKCIENDCKMMNSHFLDGNL-----VPLEGKEVDSRRMLITLNDLQKHNEKRLDQ	333	
Db	275	DPPASIELDGFYVGAE-APGELGGIGPAPARBELDASRRVITLNDLQKHNDKDLQ	333	
QY	335	LVEMANVYALSHQOKSRAFYRIQATRMWTAGNLTIKHAAQOKKASSMSVDEHPDEDEP	394	
Db	334	LVGIANTYALLHQOKSRAFYRIQATRLMTAGNVLRRAADASTRAAPABGACDE-DDG	392	
QY	395	ISKVEFDFDCSYOCLENGCAVLLTVYRKGDMSKTMVYDYKTEDGSANAGADYEFTETGV	454	
Db	393	ASRIEFEPSELHYCHENGCSVLLTVCQGEGBNSFFYDYRPFEDGSARAGSDYEVSECTLV	452	
QY	455	LKPGTQKEFESVGIIDDDIFEDDEHFPVRLSNVAITEEQ----PEECMPRAINFSLPLR	510	
Db	453	KPQGTQKELELIGIIDDDIFEDDEHFPVRLNLNVGAQGFEEDEG-----GRPK	503	
QY	511	AVLASPCAATYIIDDHAGJFTEECPTIHVSESIGVMEVYLTSGARGATVIFPRTVE	570	
Db	504	GRIVAPPLATYITIIDDDHAGJFESQDRLRLHNSCECMGIVDAVAVASSGARIVRLPYRTVD	566	
QY	571	GTANGGEDPEFDYVGELEFKNDETV	595	

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Db      564 GTACGGVHYEDACGELEFGDETM 568

|||||:|:| ||||:||||:
RESULT 11
MAC2_RAT
ID      MAC2_RAT      STANDARD:      PRF:      921 AA.
AC      P48768:
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
DE      2).
GN      SLC8A2 OR NCX2.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RN      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Brain stem;
RX      MEDLINE=94292496; PubMed=8021246;
RA      Li Z., Matsuda S., Hryshko L.V., Nicoll D.A., Beshon M.M.,
RA      Burke E.P., Lifton R.P., Philipson K.D.;
RT      "Cloning of the NCX2 isoform of the plasma membrane Na(+)-Ca2+
RT      exchanger."
RL      J. Biol. Chem. 269:17434-17439(1994).
RN      [2]
RN      TISSUE SPECIFICITY.
RP      STRAIN=Sprague-Dawley;
RC      MEDLINE=96394663; PubMed=8798769;
RX      Nicoll D.A., Quednau B.D., Qul Z., Xia Y.-R., Lusis A.J.,
RA      Philipson K.D.;
RT      "Cloning of a third mammalian Na+Ca2+ exchanger, NCX3.*;
RL      J. Biol. Chem. 271:24914-24921(1996).
CC      -I- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
CC      COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
CC      SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC      -I- ENZYME REGULATION: BY ATP.
CC      -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -I- TISSUE SPECIFICITY: BRAIN AND SKELETAL MUSCLE.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: U08141; AAA19920.1; -.
DR      InterPro: IPR003644; Calx_beta.
DR      InterPro: IPR004837; Naca_Exmemb.
DR      InterPro: IPR004836; Na_Ca_Ex.
DR      Pfam: PF01699; Na_Ca_Ex; 2.
DR      Pfam: PF03160; Calx_beta; 2.
DR      PRINTS: PR01259; NACAEXCHNGR.
DR      SMART: SM00237; Calx_beta; 2.
DR      TIGRFAMs: TIGR00845; caca; 1.
KW      transport; Antiport; Calcium transport; Sodium transport;
KW      transmembrane; Glycoprotein; Phosphorylation; signal;
KW      Calmodulin-binding; Repeat.
FT      SIGNAL      1      20      POTENTIAL.
FT      CHAIN      21      921      SODIUM/CALCIUM EXCHANGER 2.
FT      DOMAIN      21      68      EXTRACELLULAR (POTENTIAL).
FT      TRASMEM      69      90      POTENTIAL.
FT      TRASMEM      91      130      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      131      152      POTENTIAL.
FT      TRASMEM      153      164      EXTRACELLULAR (POTENTIAL).
FT      TRASMEM      165      185      POTENTIAL.
FT      DOMAIN      186      196      CYTOPLASMIC (POTENTIAL).
FT      TRASMEM      197      219      POTENTIAL.
FT      DOMAIN      220      222      EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 223 246 POTENTIAL.
FT DOMAIN 247 720 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 721 740 POTENTIAL.
FT DOMAIN 741 747 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 748 770 POTENTIAL.
FT DOMAIN 771 772 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 773 791 POTENTIAL.
FT DOMAIN 792 822 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 823 843 POTENTIAL.
FT DOMAIN 854 854 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 855 875 POTENTIAL.
FT DOMAIN 876 892 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 893 909 POTENTIAL.
FT DOMAIN 910 921 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 921 921 CALMODULIN-BINDING (BY SIMILARITY).
FT REPEAT 135 175 ALPHA-1.
FT REPEAT 397 468 BETA-1.
FT REPEAT 527 597 BETA-2.
FT REPEAT 790 826 ALPHA-2.
FT DOMAIN 29 32 POLY-PRO.
FT CARBOHYD 638 641 POLY-GLU.
FT CARBOHYD 817 817 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 817 817 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 921 AA: 100522 MW: 0CDB26BACBCE6B1 CRC64:

Query Match 60.5%; Score 1954.5; DB 1; Length 921;
Best Local Similarity 64.1%; Pred. No. 2,7e-133;
Matches 371; Conservative 92; Mismatches 91; Indels 25; Gaps 6;

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AC Q9IAL8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
exchange protein 1) (Retinal rod Na-CaK exchanger).
GN SLC24A1 OR NCKX1.
OS Gallus gallus (Chicken).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20130359; PubMed=10662833;
RX Prinsen C.F.M., Szecsenyi R.T., Schneckamp P.P.M.;
RT Molecular cloning and functional expression of the potassium-
dependent sodium-calcium exchanger from human and chicken retinal cone
photoreceptors.
RT J. Neurosci. 20:1424-1434(2000).
RL J. Neurosci. 20:1424-1434(2000).
CC -!- FUNCTION: Critical component of the visual transduction cascade,
controlling the calcium concentration of outer segments during
light and darkness. Light causes a rapid lowering of cytosolic
free calcium in the outer segment of both retinal rod and cone
photoreceptors and the light-induced lowering of calcium is caused
by extrusion via this protein which plays a key role in the
process of light adaptation. Transports one Ca(2+) and one K(+) in
exchange for four Na(+).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Retinal rods. Localizes to the inner segment
of rod photoreceptors.
CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF177984; AAF25808.1; -
DR InterPro: IPR004817; K_NaCaexchng.
DR InterPro: IPR004817; K_NaCaexchng.
DR InterPro: IPR004837; NaCa_Exmemb.
DR Pfam: PF01699; Na_Ca_Ex. 2.
DR TIGRfams: TIGR00367; K_NaCaexchng-rel. 1.
DR TIGRfams: TIGR00927; 2A1904; 1.
KW Vision; Transport; Antipport; Symport; Calcium transport;
KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
KW Phosphorylation; Signal; Repeat.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 663 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT DOMAIN 32 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 149 POTENTIAL.
FT DOMAIN 150 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 194 POTENTIAL.
FT DOMAIN 195 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 221 POTENTIAL.
FT DOMAIN 222 228 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 229 253 POTENTIAL.
FT DOMAIN 254 259 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 260 276 POTENTIAL.
FT DOMAIN 277 471 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 472 492 POTENTIAL.
FT DOMAIN 493 499 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 500 520 POTENTIAL.
FT DOMAIN 521 535 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 536 556 POTENTIAL.
FT DOMAIN 557 574 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 575 595 POTENTIAL.
FT TRANSMEM 596 604 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 605 625 POTENTIAL.
 FT DOMAIN 626 632 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 633 653 POTENTIAL.
 FT DOMAIN 654 663 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 170 210 ALPHA-1.
 FT REPEAT 543 574 ALPHA-2.
 FT MOD_RES 337 337 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 663 AA; 73771 MW; D624E3080C43082 CRC64;

Query Match 6.5%; Score 209.5; DB 1: Length 663;
 Best Local Similarity 21.9%; Pred. No. 1.7e-07;
 Matches 124; Conservative 74; Mismatches 166; Indels 203; Gaps 26;

OY 77 VIVFVALIYMLGVSIADR-FMASIEVTSQEREVTIKKNGESTTTIRNMEVSN 135
 b 131 VVLHFGMMVYVALAIYDEYFVALGVTEK-----LGI-SEDAVG 172
 OY 136 LTLMASSAPRILSLIEVCGHFLA-GDLCPSTIVSAAFMFLIGICVYVDPGET 194
 Db 173 AFPMAGSAPRLFTSLIGV-----FISHSNVIGITVGSAPVNIIFVIGTCLF-----S 223
 OY 195 RKIKHARVETFAAMSIFAYIWL-----MILAVSPGVYVMEGLTFEPVCV----- 245
 Db 224 RRLIHL-----TWWPLRFDISFYVDLMLFLFDSYIDMWESILLITAYATVFTMK 277
 OY 246 ---LLAVVADK-----RLLFYKYMKKYRTDKHNGIILETGDHDKGIEMDGKM- 292
 Db 278 HNVSLQWVKELSKKLNAVQAASAEHMRK-----SSVAVAEQGTFR-----ADGKKLQ 327
 OY 293 -----NS-----HFLDGNLVPLEKGEVDSRRRMITLADLAK 326
 Db 328 PTTALQRTSSASLHNSQMRSTIFQMLHTLD-----PLAGAF-----KRVILSLIAEV 379
 OY 327 HPEKDLQLEVMANYALSHQOKRAFYRIQATRMWTGAGNLIKHAQOAKKASSMSV 386
 Db 380 KADS-----LTGGT-----KPEAEERQASQ----- 401
 OY 387 HTDEPDLISKVFDPDPCSYQLENCGAVLLTVRRKGDMSTMYDYKTEDSANAAGDY 446
 Db 402 -----NTQVMPAS-----DSEPSKQKQEDTPQDQOPSD- 434
 OY 447 EFTGTVLAKPEQOKEPSVGIIDDIPEDEHFFVRLSNVLEEQPEEGPRAFNEL 506
 b 435 -----NSSESSSSEDDSDSDSTDEE-----NDEPLSLEWPTRRKQAIYFL 478
 OY 507 PLPRAVLASPCVAVYITL---DDHAGITFECDTI-----HYSESIGVME 549
 Db 479 -FP---IYFPLMSTIPDVANPDSKKEFVITTFGSIITWIAFSYLMVMAHQVGETIGISE 534
 OY 550 VKVLTSGARGTIVFPRTVEGTANG 576
 Db 535 EIMGLTIIAAGTSIPDLITSVIAVRKG 561

RESULT 13
 NKX2_HUMAN
 ID NKX2_HUMAN STANDARD; PRT; 661 AA.
 AC O9U140; O9NZ04; O9NTN5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/potassium/calcium exchanger 2 precursor (Na(+)/K(+)/Ca(2+)-
 exchange protein 2) (Retinal cone Na-Ca+K exchanger).
 GN SLC24A2 OR NKX2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE-Retina;
 RX MEDLINE=20130359; PubMed=10662833;
 RA Prinsen C.F.M., Szerencsei R.T., Schetkamp P.P.M.;
 RT "Molecular cloning and functional expression of the potassium-
 dependent sodium-calcium exchanger from human and chicken retinal cone
 photoreceptors";
 RT J. Neurosci. 20:1424-1434(2000).
 RL [2]
 RN SEQUENCE OF 311-376 FROM N.A. (ISOFORM 1).
 RP Subra H.;
 RA Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 RL
 CC -1- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC
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 CC -----

DR EMBL: AF097366; AAF21810.1; -
 DR EMBL: AF177987; AAF25811.1; -
 DR EMBL: AL133281; CAB92751.2; -
 DR Genew: HGNC:10976; SLC24A2.
 DR InterPro: IPR004481; K_NaCaexchg.
 DR InterPro: IPR004837; NaCa_Extmb.
 DR Pfam: PF01699; Na-Ca_Ex_3.
 DR TIGRFAMS: TIGR00367; K_NaCaexchang-rel; 1.
 DR Vision; Transport; Antipor; Symport; Calcium transport;
 KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
 KW Signal; Repeat; Alternative splicing.
 FT SIGNAL 1
 FT CHAIN 59 661
 FT DOMAIN 59 132 SODIUM/POTASSIUM/CALCIUM EXCHANGER 2.
 FT TRANSMEM 133 153 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 154 178 POTENTIAL.
 FT TRANSMEM 179 199 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 200 204 POTENTIAL.
 FT TRANSMEM 205 225 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 226 243 POTENTIAL.
 FT TRANSMEM 244 264 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 265 265 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 266 286 POTENTIAL.
 FT DOMAIN 287 469 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 470 490 POTENTIAL.
 FT DOMAIN 491 497 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 498 518 POTENTIAL.
 FT DOMAIN 519 533 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 534 554 POTENTIAL.
 FT DOMAIN 555 569 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 570 580 POTENTIAL.
 FT DOMAIN 591 602 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 603 623 POTENTIAL.
 FT DOMAIN 624 630 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 631 651 POTENTIAL.
 FT TRANSMEM 652 661 POTENTIAL.
 FT REPEAT 174 214 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 341 372 ALPHA-1.
 FT REPEAT 541 572 ALPHA-2.
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 376 MISSING (IN ISOFORM 2).
 FT VARSPLIC 360
 SQ SEQUENCE 661 AA; 73663 MW; E6359C1F95C3AB3E CRC64;

Query Match 6.3%; Score 203.5; DB 1; Length 661;
 Best Local Similarity 22.3%; Pred. No. 4.6e-07;
 Matches 128; Conservative 91; Mismatches 204; Indels 151; Gaps 28;

QY 39 PSCONNESGSSGSDCEGVLPIWPENP-SLCD-KIARIYVYFVALTIMFEGVSIAD 96
 DB 101 PPLSKBES-ENSTDHOGD---YPKDIFSEERRKGAIIHVIOMITFIALALVCD 154
 QY 97 R-FMASEIVITSOBREVITIKKPNGETSTTIRVNEFVSNLTALGSSAPEILLSTIEV 155
 DB 155 EEFVPSLVTITEK-----LGI-SDDVACATFMAAGSAPBELFTSLIGV 196
 QY 156 CGHGFLA-GDLGPSTIVGSAFNNFTITGICVYVYIPDGETRKIKHLVFEFTAAMSIFAY 214
 DB 197 ---FIHNVNIGTIVGSAVFNFILVIGMCALF---SREILNL-----TWPPLFRD 241
 QY 215 IWLX-----MILAVSPGVQVWEGLLT-FFPPVCYL-----AVVADKRLIFKYM 261
 DB 242 VSEFIVDLMLIFELDNVIMMESLILLAYFCYVVEKFNVOVEKVV--KOMINENKV 299
 QY 262 HKKVRTDKHNGIIEETGDPH---KGIEMDGKMNNSH--FLDGNLVPLEGREVDESRR 314
 DB 300 VKYAPAPAOAKPSARCKDEPTLPARKRLORGSSASLHNSLMNSIFOL----- 349
 QY 315 EMIRILKDLKQHPKDLQDLEMANYYALSHOOKSRAPYRIQATRMGTAGNLLKKHAA 374
 DB 350 -MHTLDPLAE-----ELGSGYKLYXD-----TWTEGREPREKASI 385
 QY 375 --EQAKKASSMEVHTDEPE-----DFISKVFPPDPCSTOCLENGCVALLTVARKGDMS 426
 DB 386 LHKIAKK---KCHVDENRONGAMNHVERKIELPNSTSDVENTPSSDSEPVQONNLS 440
 QY 427 KTMVVDKTEDGSANAGADEETEGTVVLKPGTOKFEFSGIIDDQFEEDHEFVRLSN 466
 DB 441 HNT-----EGAPAQADEEDQPLSLAMPSETRKQVTLVIFPVFP---LWITLPD 489
 QY 487 VRIEEQPEEGMPALFNSLPLPRAVLASPCVATVITLDDHAGIFTECDTI---HVS 542
 DB 490 VR--KPSRRKFFPTFGSI-----TWIAVESFLVMWMAHQV 525
 QY 543 ESTGVMEVKVLRNLSGAGTYIVPRVVEGTAKG 576
 DB 526 ETGISSEIMGLTLLAGTSLPDLTISVIARKG 559

RESULT 14
 NKX1_RAT STANDARD; PRT; 1181 AA.
 ID NKX1_RAT STANDARD; PRT; 1181 AA.
 QY 09QZM6; 062932;
 15-JUN-2002 (Rel. 41, Created)
 15-JUN-2002 (Rel. 41, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-
 exchange protein 1) (Retinal rod Na-Ca+K exchanger).
 GN SLC24A1 OR NKX1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC MBLTaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN-Sprague-Dawley; TISSUE-Eye;
 RX MEDLINE=20217335; PubMed=10751314;
 RA Poon S., Leach S., Li X.-F., Tucker J.E., Schneckamp P.P.M.,
 RT "Alternatively spliced isoforms of the rat eye
 sodium/calcium/potassium exchanger NKX1.";
 RL Am. J. Physiol. 278:C651-C660(2000).
 RN [2]
 RP SEQUENCE OF 1067-1155 FROM N.A.
 RA White K.E., Gesek F.A., Friedman P.A.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

CC - FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here) 2, 3 and 4; are
 CC produced by alternative splicing.
 CC - TISSUE SPECIFICITY: Highly expressed in the eye.
 CC - SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC
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 CC
 CC EMBL: AF176688; AAD53121.1; -
 CC EMBL: U49235; AAB37753.1; -
 CC InterPro: IPR004817; K_NaCaexchang.
 CC InterPro: IPR004481; K_NaCaexchng.
 CC InterPro: IPR004837; NaCa_Exmemb.
 CC Pfam: PF01699; Na_Ca_Ex; 3.
 CC TIGRPFAM: TIGR00367; K_NaCaexchang-rel; 1.
 CC TIGRPFAM: TIGR00927; 2A1904; 1.
 CC Vision; Transport; Antiport; Symport; Calcium transport;
 CC Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;
 CC Alternative splicing.
 CC
 CC SIGNAL 1 38
 CC CHAIN 39 1181
 CC DOMAIN 39 419
 CC TRANSMEM 420 440
 CC DOMAIN 441 464
 CC TRANSMEM 465 485
 CC DOMAIN 486 491
 CC TRANSMEM 492 512
 CC DOMAIN 513 519
 CC TRANSMEM 520 544
 CC DOMAIN 545 552
 CC TRANSMEM 553 569
 CC DOMAIN 570 989
 CC TRANSMEM 990 1010
 CC DOMAIN 1011 1017
 CC TRANSMEM 1018 1038
 CC DOMAIN 1039 1053
 CC TRANSMEM 1054 1074
 CC DOMAIN 1075 1092
 CC TRANSMEM 1093 1113
 CC DOMAIN 1114 1121
 CC TRANSMEM 1122 1142
 CC DOMAIN 1143 1150
 CC TRANSMEM 1151 1171
 CC DOMAIN 1172 1181
 CC REPEAT 461 501
 CC REPEAT 1061 1092
 CC DOMAIN 730 905
 CC REPEAT 730 741
 CC REPEAT 742 754
 CC REPEAT 755 766
 CC REPEAT 767 778
 CC REPEAT 779 791
 CC REPEAT 792 804
 CC REPEAT 805 817
 CC REPEAT 818 830
 CC REPEAT 831 843
 CC REPEAT 844 856
 CC REPEAT 857 869
 CC REPEAT 870 881

1. 14 X APPROXIMATE TANDEM REPEATS.
 2.
 3.
 4.
 5.
 6.
 7.
 8.
 9.
 10.
 11.
 12.

FT REPEAT 882 893 13.
 FT REPEAT 894 905 14.
 FT DOMAIN 952 974 POLY-GLU.
 FT MOD_RES 625 625 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHD 271 271 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT VASAPPLIC 598 710 MISSING (IN ISOFORM 2).
 FT VASAPPLIC 616 710 MISSING (IN ISOFORM 3).
 FT VASAPPLIC 652 679 MISSING (IN ISOFORM 4).
 SO SEQUENCE 1181 AA; 129980 MW; B063C1C1193696AE CRC64;
 Query Match 6.3%; Score 203; DB 1; Length 1181;
 Best Local Similarity 20.7%; Pred. No. 1.le-06;
 Matches 134; Conservative 89; Mismatches 207; Indels 216; Gaps 29;
 Oy VIVYVALVLMELGSIADR-FMASIEVITSGEREVITKKNGETSTTTIVMNETSN 135
 Db 422 VVLMFGMTYFVALVAYCDEYFVALGYTDK-----LQI-SEDAVG 463
 Y 136 LTLMAIGSSAPRLLSLIEVCGHGFIA-GDLGPTTVGSAPAFMFIIGICVYVIPDGET 194
 Db 464 ATFMAGGSAPRLLSLIGV-----FISHSNVIGITVGSANVILFVICTALF-----S 514
 Oy 135 RKIKLRVFTTAANSIFAYWLY-----MLAVSPGVVYEGLLTLEFPVGV---- 245
 Db 515 REILNL-----TWMPLEFRDVSFYLLDLSMLIVFLDSLIAWESLLLLALVALVYTMK 568
 Oy 246 ----LLAVADK--RLLYKYMKKRYRDKHNGIITETGHPKGIEM-----DGK 290
 Db 569 WNKQIERVWKQESRRPAKVVALDLSKPSDGALEENQDNKKLKLPSVLTGRSSSAS 628
 Oy 291 MNNS-----HFLDGNLVL-----EGKEVDESREMIIRLEKDK-----OKHP----- 328
 Db 629 LHNSTIIRSTYIHLMLHSLDPLGEARPSKDKQESLNGEARVLPQTAESSDEEFAELPA 688
 Oy 329 -----EKIDQLEVANYALSHQOKSAFYRIQATPMTGACN 367
 Db 689 VYVTPAPARPDKQDEEDPCQEDVDVAENRGMGTGEEGERETA---EGKKDEGETE 744
 Oy 368 ILKRIAAQAKKASSMSEVNHDEPEDFISKVFDFPCSYQCLENCAGVLLTVRKGDMSK 427
 Db 745 AERKDDGDEETETGKKEGEGETES-----EGKRD----- 774
 Oy 428 TMVYDYKTEDGSANAGAYE---FTEGVVYLKPGETOKEFSGIIDDIFE----- 475
 Db 775 ----EQBETEAEGKADHEGETEADEKVEHEGETEA---GTEDDEGGETEAEGKEVE 827
 Y 476 -----EDEHFFVRLSNVRIEEOPE---EGMPRAIFNSPLPRAVLASPCVATVT 522
 Db 828 QEGETEAEGKEVEH-----EVETEAREKRETNHEGETAECK----- 863
 Oy 523 ILDDHAGITFEECTIH--VSESIGVMEVKVLRITSGARGIYVPRYVEGTAKGGEDF 580
 Db 864 --EADHEGETEAEGVNEQGETEAEGKVEHEGETAEGED-----EHEGSESTQADDT 914
 Oy 581 E--DTYGELEFNDETVCROFADYGRGG-----QEDSHD 614
 Db 915 EVKQDEGEAE-ANADQCEFAEGKADGGSGSDGDSDEEDED 959
 RESULT 15
 NKX2_RAT STANDARD: PRT: 670 AA.
 AC OS4701: OS4706:
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/potassium/calcium exchanger 2 precursor (Na(+)/K(+)/Ca(2+)-
 exchange protein 2) (Retinal cone Na-Ca+K exchanger).
 GN SLC24A2 OR NKX2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=96128630; PubMed=9461611;
 RA Tsol M., Rhee K.-H., Bungard D., Li X.-F., Lee S.-L., Auer R.N.,
 RA Lytton J.;
 RT "Molecular cloning of a novel potassium-dependent sodium-calcium
 RT exchanger from rat brain".
 RL J. Biol. Chem. 273:4155-4162(1998).
 CC -1- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Expressed abundantly in all regions of the
 CC brain and weakly in the eye, large intestine and adrenal tissue.
 CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL: AF021923; AAC19405.1; -;
 DR EMBL: AF027506; AAC19404.1; -;
 DR InterPro: IPR004481; K_NacCaexchg.
 DR InterPro: IPR004837; Naca_Exmemb.
 DR Pfam: PF01699; Na_Ca_Ex_2.
 DR TIGRfams: TIGR00367; K_NacCaexchang-rel; 1.
 KM Vision; Transport; Antiport; Symport; Calcium transport;
 KM Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
 KM Signal; Repeat; Alternative splicing.
 FT SIGNAL 1 58
 FT CHAIN 59 670
 FT DOMAIN 1 133
 FT TRANSSEM 134 154
 FT DOMAIN 155 179
 FT TRANSSEM 180 200
 FT DOMAIN 201 205
 FT TRANSSEM 206 226
 FT DOMAIN 227 244
 FT TRANSSEM 245 265
 FT DOMAIN 266 266
 FT TRANSSEM 267 287
 FT DOMAIN 288 478
 FT TRANSSEM 479 499
 FT DOMAIN 500 506
 FT TRANSSEM 507 527
 FT DOMAIN 528 542
 FT TRANSSEM 543 563
 FT DOMAIN 564 578
 FT TRANSSEM 579 599
 FT DOMAIN 600 611
 FT TRANSSEM 612 632
 FT DOMAIN 633 639
 FT TRANSSEM 640 660
 FT DOMAIN 661 670
 FT REPEAT 175 215
 FT REPEAT 550 581
 FT CARBOHD 112 112
 FT VASAPPLIC 360 376
 FT CONFLICT 309 309
 SQ SEQUENCE 670 AA; 74656 MW; 4EB55467FC6679E CRC64;

Query Match 6.2%; Score 201.5; DB 1; Length 670;
Best Local Similarity 24.8%; Pred. No. 6.6e-07;
Matches 104; Conservative 69; Mismatches 127; Indels 119; Gaps 25;

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QY 39 PSTGQNNESGSSDCKEGVILFIWYENP-SIGD-KIARIYVFVALIYMFGLVSIAD 96
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 102 PPASQEDRSRNG-TDHAQGD----YPKDVSLEERRKGAIIILHVGIMYMFALAIYCD 155
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 R-FMASIEVITTSQREVTIKKPNGETSTTIRVWNETVSNLTLMALGSSAPEILLSEIV 155
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 EFVVPSTLVITER-----LGI-SDVAGATFMAAGSAPELFTSLIGV 197
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 156 CGHGPIA-GDLGPTIVGSAFNMFIIGICVYVIPDGETRKIKHLRVEFTAMSIYAY 214
   || : : || : : || : : || : : || : : || : : || : : || : : ||
Db 198 ----FIHSHVIGIGTIVGSAVFNILEVIGCALF-----SREILNL-----TWMPLEFRD 242
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 215 IMLY-----MILAVFSRGVYQVWEGLLTLFFFPVCVILLAVADKRLLFYKMHKKYRTDK 269
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 VSFYIVDLMLILFFLDNVIIMWESLL-----LITAYFA--YVFEKFNQVERWVK 292
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 270 ---HRCIIE-----TEGD-----HPKGIEMDGK-----MMNS----- 294
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   293 QMINRNKVVAVTVYSEAGAKASTAGDKEEPTLPKPKRLQBGSSASLHNSLIRNSIFOLMI 352
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 HFLDGNLVPLE-----GK-----EYDESR-REMIRILKDLKOKHPEKDDQ---LVE 337
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 353 HTLD---PLAEELGSYGKLYYDTWTEGFREREKASILHKIAKKKQVDENERONGCAN 408
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 MANYVALSHQOKSRATYRIQATRMTCG-----GNILKHAAEQAKKASSMSEVHTDEP 391
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 409 HVDYAAEKIELPNSTSTEVETPSSSEASEPVGNGNLSHSIEADAPQATETAEEDDQP 467
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Search completed: November 30, 2002, 12:29:00
Job time : 13.2654 secs